

Claims with Markings to Show Changes

At page 1, delete the third paragraph (lines 12-14).

At page 1, line 5, before "Statement" insert the following paragraph:

Reference to Related Applications.

This application is a continuation-in-part of PCT/US98/10080, filed May 15, 1998, which is a continuation-in-part of U.S.S.N. 08/888,534, filed July 7, 1997, and U.S.S.N. 08/857,076, filed May 15, 1997, issued as U.S. Patent No. 6,225,120 on May 1, 2001.

At page 83, replace the second paragraph (lines 14-26) with the following replacement paragraph:

Score = 151 (68.4 bits), Expect = 1.9e-140, Sum P(8) = 1.9e-140
Identities = 28/54 (51%), Positives = 38/54 (70%)

SEQ_ID NO: 161 AFX:226 SPVGHFAKWSGSPCSRNRREEADMWTTFRPRSSNASSVSTRLSPLRPESEVLAE279
SEQ_ID NO: 162 SP F+KW SP S + ++ D W+TFRPR+SSNAS++S RLSP+ E + L E
SEQ_ID NO: 163 FKHR:287 SPGSQFSKWPASPGSHSNDDFDNWSTFRPRTSSNASTISGRLSPIMTEQDDLGE340
SEQ_ID NO: 164 DAF-16a SFRPRTQSNL SIPGSSS

Score = 132 (59.8 bits), Expect = 1.9e-140, Sum P(8) = 1.9e-140
Identities = 22/42 (52%), Positives = 28/42 (66%)

SEQ_ID NO: 165: AFX: 7 KAAAIIDLDPDFEPQSRPRSCTWPLPRPEIANQPSEPPEVEP 48
SEQ_ID NO: 166 +A+++DPD FEP RPRSCTWPLPRPE + S P
SEQ_ID NO: 167 FKHR: 3 EAPQVVEIDPDFEPLPRPRSCTWPLPRPEFSQNSATSSPAP 44
SEQ_ID NO: 168 DAF-16 TFMNTPDDVMNNDDMEPIPRDRCNTWPMRRPQLEPPLNSSP 177
SEQ_ID NO: 169 T ++P+ V ++ D EP+PR R TWP+ RP++ + ++++

Beginning at page 97, please replace page 97, second paragraph (lines 3-37), page 98, page 99, and page 100, first paragraph (lines 1-4) with the following replacement paragraphs.

Score = 252 (88.7 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 47/80 (58%), Positives = 60/80 (75%), Frame = +3

SEQ ID NO:170 Query: 439 LEKQAGGNPWHQFVENNLILKMGPVDKRKGFLARRRQLLTEGPHLYVDPVNKVLKGEI 498
SEQ ID NO:171 LE+Q NP+H F N+LILK G ++K++GLFARRR LI+TEGPHL Y+D N VLKGE+
SEQ ID NO:172 Sbjct: 1818 LEEQRVKNPFHIFTNNSLILKQGYLEKKRGLFARRRMFLLTEGPHLLYIDVPNLVLKGEV1997

SEQ ID NO:170 Query: 499 PWSQELRPEAKNFKTFFVHT 518
SEQ ID NO:171 PW+ ++ E KN TFF+HT
SEQ ID NO:172 Sbjct: 1998 PWTPCMQVELKNSGTFFIHT 2057

Score = 201 (70.8 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 48/123 (39%), Positives = 72/123 (58%), Frame = +1

SEQ ID NO:173 Query: 263 SDLWALGCIIYQLVAGLPPFRAGNEYLIFQKIIKLEYDFPEKFFPKARDLVEKLLVLDAT 322
SEQ ID NO:174 +D+W LGCI++Q +AG PPFRA N+Y + ++I +L++ FPE F +A +++ K+LV
SEQ ID NO:175 Sbjct: 802 TDIWGLGCILFQCLAGQPPFRAVNQYHLLKRIQELDFSPPEGFPPEEASEIIAKILV--G*H 978

SEQ ID NO:173 Query: 323 KRLGCE----EMEGYGP-----LKAHPFFESVTWENLHQQTTPKLTAYLPAMSEDE 370
SEQ ID NO:174 + L E ++ P L AH FFE+V W N+ PP L AY+PA + E
SEQ ID NO:175 Sbjct: 979 ETLKTEYVIFNLQVRDPSTRITSQELMAHKFFENVDWVNIAKPPVLIAYIPATFGEPE1158

SEQ ID NO:173 Query: 371 DCYGN 375
SEQ ID NO:174 Y N
SEQ ID NO:175 Sbjct: 1159 -YSN 1170

Score = 180 (63.4 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 31/72 (43%), Positives = 52/72 (72%), Frame = +2

SEQ ID NO:176 Query: 157 FGLSYAKNGELLKYIRKIGSFDETCTRFYTAEIVSALEYLHGKGIIRDLKPENILLNED 216
SEQ ID NO:177 F + +NG+L + + GSFD ++F+ +EI++ L++LH I+HRD+KP+N+L+ +D
SEQ ID NO:178 Sbjct: 287 FVIGLVENGDILGESLCHFGSFDMLTSKFFASEILTGLQFLHDNKIVHRDMKPDNVLIQKD 466

SEQ ID NO:176 Query: 217 MHIQITDFGTAK 228
SEQ ID NO:177 HI ITDFG+A+
SEQ ID NO:178 Sbjct: 467 GHILITDFGSAQ 502

Score = 83 (29.2 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 15/53 (28%), Positives = 32/53 (60%), Frame = +

SEQ ID NO:179 Query: 108 YAIKILEKRHIKENKVPYVTRERDVMRSRLD----HPFFVKLYFTFQDDEKL 155
SEQ ID NO:180 +A+K+L+K ++ + K+ + RE++++ L HPF +LY F D ++
SEQ ID NO:181 Sbjct: 8 FAVKVLUQSKSYLNRHQKMDAIIREKNILTYLSQECGGHPFVTQLYTHFHDQARI 166

Score = 81 (28.5 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 15/29 (51%), Positives = 19/29 (65%), Frame = +2

SEQ ID NO:182 Query: 519 PNRTYYLMDPSGNNAHKWCRKIQEVRQRY 547
SEQ ID NO:183 PNR YYL D A +WC+ I +V R+RY
SEQ ID NO:184 Sbjct: 2129 PNRVYYLFDLEKKADEWCKAINDV-RKRY 2212

Score = 78 (27.5 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 15/25 (60%), Positives = 18/25 (72%), Frame = +3

SEQ ID NO:185 Query: 232 PESKQARANSFVGTAQYVSPPELLTE 256
SEQ ID NO:186 PE AR +FVGTA YVSPE+L +
SEQ ID NO:187 Sbjct: 660 PEENTARRTTFVGTLALYVSPPEMLAD 734

Overall, *C. elegans pdk-1* exhibits the following homology to human PDK-1.

Score = 118 (54.4 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 21/62 (33%), Positives = 41/62 (66%)

SEQ ID NO:188 Query: 63 KRTSNDMFQLQSMGEGAYSQVFRCREVATDAMFAVKVLQKSYLNRHQKMDAIIREKNILT 122
SEQ ID NO:189 K+ DF F + +GEG++S V RE+AT +A+K+L+K ++ + K+ + RE+++++
SEQ ID NO:190 Sbjct: 76 KKRPEDFKFGKILGEGSFSTVVLARELATSRREYAIKILEKRHIIKENKVPYVTRERDVMS 135

SEQ ID NO:188 Query: 123 YL 124
SEQ ID NO:189 L
SEQ ID NO:190 Sbjct: 136 RL 137

Score = 230 (106.0 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 39/90 (43%), Positives = 63/90 (70%)

SEQ ID NO:191 Query: 131 HPFVTQLYTHFHDQARIYFVIGLVENGDLGESLCHFGSFDMITSKFFASEILTGLQFLHD 190
SEQ ID NO:192 HPF +LY F D ++YF + +NG+L + + GSFD ++F+ +EI++ L++LH
SEQ ID NO:193 Sbjct: 139 HPFFVKLYFTFQDDEKLYFGLSYAKNGELLYKIRKIGSFDETCTRFYTAEIVSALEYLHG 198

SEQ ID NO:191 Query: NKIVHRDMKPDNVLIQKDGHLITDFGSAQ 220
SEQ ID NO:192 I+HRD+KP+N+L+ +D HI ITDFG+A+
SEQ ID NO:193 Sbjct: KGIIHRDLKPENILNEDMHIQITDFGTAK 228

Score = 238 (109.7 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 43/98 (43%), Positives = 67/98 (68%)

SEQ ID NO:194 Query: 259 EENTARRTTFVGTLALYVSPPEMLADGDVGPQTDIWGLGCILFQCLAGQPPFRAVNQYHLLK 318
SEQ ID NO:195 E AR +FVGTA YVSPE+L + +D+W LGCI++Q +AG PPFRA N+Y + +
SEQ ID NO:196 Sbjct: 233 ESKQARANSFVGTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQ 292

SEQ ID NO:194 Query: 319 RIQELEDFSFPEGFPPEEASEIIAKILVRDPSTRITSQEL 356
SEQ ID NO:195 +I +L++ FPE F +A +++ K+LV D + R+ +E+
SEQ ID NO:196 Sbjct: 293 KIKLEYDFPEKFFPKARDLVEKLLVLDATKRLGCEEM 330

Score = 85 (39.2 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 17/35 (48%), Positives = 21/35 (60%)

SEQ ID NO:197 Query: 356 LMAHKFFENWDWVNIAKPPVLHAYIPATFGEPE 390
SEQ ID NO:198 L AH FFE+V W N+ PP L AY+PA + E
SEQ ID NO:199 Sbjct: 336 LKAHPFFESVTWENLHQQTTPKLTAYLPAMSEDDE 370

Score = 324 (149.3 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 59/104 (56%), Positives = 75/104 (72%)

SEQ ID NO:200 Query: 458 LEEQRVKNPFHIFTNNSLILKQGYLEKKRGLFARRRMFLLTGPHLLYIDVPNLVLKGEV 517
SEQ ID NO:201 LE+Q NP+H F N+LILK G ++K++GLFARRR LLTEGPHL Y+D N VLKGE+

SEQ ID NO:202 Sbjct: 439 LEKQAGGNPWHQFVENNLILKMGPVDKRKGLFARRRQLLLTEGPHLYYDPVNKVLKGEI 498

SEQ ID NO:200 Query: 518 PWTPCMQVELNSGTFFIHTPNRVYYLFDEKKADEWCKAINDV 561
SEQ ID NO:201 PW+ ++ E KN TFF+HTPNR YYL D A +WC+ I +V
SEQ ID NO:202 Sbjct: 499 PWSQELRPEAKNFKTFFVHTPNRTYYLMDPSGNNAHKWCRKIQEV 542

Mapping of the *mg142* mutation to this open reading frame establishes the function of this protein. It is much more closely related to PDK than to any other known kinase. PDK is a mammalian kinase that phosphorylates an essential serine residue on AKT, contributing to its activation. The region of *akt-1* phosphorylated by PDK-1 is shown below (SEQ ID NO: 203-207, and 305).

SEQ ID NO:203 human AKT 276 KLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEV 320
SEQ ID NO:204 KLENL+LDKGHIKI DFGLCKE I G TFCGTPEYLAPEV
SEQ ID NO:205 Ce akt-1 33509 KLENLLDKDGHIKIADFGLCKEEISFGDKTSTFCGTPEYLAPEV 33643

SEQ ID NO:206 Ceakt2 326 LCKEEIKYGDKTSTFCGTPEYLAPEVIEDIDYDRSDWWGVGVVYEMMCGR LPFSAKENGK
SEQ ID NO:207 LCKE I G TFCGTPEYLAPEV+ED DYR+VDWWG+GVV MYEMMCGR LPF ++++
SEQ ID NO:305 moAkt: 298 LC KEGISDGATMKTFCGTPEYLAPEVLEDNDYGRAV DWWGLGVV YEMMCGR LPF YNQDHER

Replace page 178, fourth paragraph, lines 21-24, page 179-186, and page 187, first paragraph, lines 1-14, with the following replacement paragraphs:

Pepck

>R11A5

Length = 26,671

Plus Strand HSPs:

Score = 994 (461.5 bits), Expect = 0.0, Sum P(5) = 0.0
Identities = 176/223 (78%), Positives = 195/223 (87%), Frame = +1

SEQ ID NO:211 Query:201 AKNNGEFVRCVHSVGQPKPVATKVINHWPCNPEKTIIAHRPAEREIWSFGSGYGGNSLLG 260
SEQ ID NO:212 A N +FVRC+HSV G P+PV +VINHWPCNPE+ +IAHPR EREIWSFGSGYGGNSLLG
SEQ ID NO:213 Sbjct:8682 ALGNQDFVRCIHSVGLPRPVKQRVINHWPCNPERVLIAHPPEREIWSFGSGYGGNSLLG 18861

SEQ ID NO:211 Query: 261 KKCFALRIAMNIGYDEGWMAEHMLIMGVTS PKGEERFVAAAFPSACGKTNLAMLEPTI PG 320
SEQ ID NO:212 KKCFALRIA NI DEGWMAEHMLIMGV T P G E F+AAAFPSACGKTNLAMLEPT+PG
SEQ ID NO:213 Sbjct:18862 KKCFALRIASNIAKDEGWMAEHMLIMGVTRPCGREHFIAAAFPSACGKTNLAMLEPTLPG 19041

SEQ ID NO:211 Query: 321 WKVRVIGDDIAWMKFGADGR LYAINPEYGGFGVAPGTSKTNPMAMASFQENTIFTNVAE 380
SEQ ID NO:212 WKVR +GDDIAWMKFG DGR LYAINPE GFFGVAPGTS+KTNPMA+A+FQ+N+IFTNVAE
SEQ ID NO:213 Sbjct:19042 WKVRCVGDDIAWMKFGEDGR LYAINPEAGFFVAPGTSNKTNPMAVATFQKNSIFTNVAE 19221

SEQ ID NO:211 Query: 381 TADGEYFWEGLEHEVKNPVDMINWLGE PWHIGDESKAHPNS 423
SEQ ID NO:212 TA+GEYFWEGLE E+ + VD+ WLGE WHIG+ AAHPNS
SEQ ID NO:213 Sbjct: 19222 TANGEYFWEGLEDEIADKNVDITTLGEKWHIGEPGVAAHPNS 19350

Score = 657 (305.1 bits), Expect = 0.0, Sum P(5) = 0.0
Identities = 120/173 (69%), Positives = 144/173 (83%), Frame = +1

SEQ ID NO:214 Query: 32 KGDFVSLPKHVQRFVAEKAELMKPSAIFICDGSQNEADELIARCVERGVLVPLKAYKNY 91
SEQ ID NO:215 +GDF LP VQRF+AEKAELM+P IFICDGSQ+EADELI + +ERG+L L+AY+NNY
SEQ ID NO:216 Sbjct:18181 QGDFHLLPAKVQRFIAEKAELMRPRGIFICDGSQHEADELIDKLIERGMLSKEAYENNY 18360

SEQ ID NO:214 Query: 92 LCRTDPRDVARVESKTWMITPEKYDSVCHTPEGVKPMGGQWMSPDEFKGKELEDDRFPGCMA 151
SEQ ID NO:215 +CRTDP+DVARVESKTWM+T KYD+V HT EGV+P+MG W++P++ ELD RFPGCMA
SEQ ID NO:216 Sbjct:18361 ICRTDPKDVARVESKTWMVTNKYDTVTHTKEGVEPIMGHWLAPEDLATELDSRFPGCMA 18540

SEQ ID NO:214 Query: 152 GRIMYVIPYSMGPVGGLSKIGIELTDSDYVVLCMRIMTRMGEPVLKALAKNN 204
SEQ ID NO:215 GR MYVIP+SMGPVGGLSKIGI+LTDS+YVVL MRIMTR+ V AL +
SEQ ID NO:216 Sbjct: 18541 GRIMYVIPFSMGPVGGLSKIGIQLTDSNYVVLSMRIMTRVNNDVWDALGNQD 18699

Score = 453 (210.3 bits), Expect = 0.0, Sum P(5) = 0.0
Identities = 77/107 (71%), Positives = 90/107 (84%), Frame = +1

SEQ ID NO:217 Query: 424 RFTAPAGQCPIIHDPDWEKPEGVPIDAIIFGGRRPEGVPLVFESRSWVHGIFVGACVKSEA 483
SEQ ID NO:218 RF APA QCPIIHPDWE P+GVP+AIIFGGRR+GVPL++E+ SW HG+F G+C+KSEA
SEQ ID NO:219 Sbjct:19396 RFAAPANQCPPIIHPDWESPQGVPIEAIIFGGRRPQGVPILYETNSWEHGVTGSCLKSEA 19575

SEQ ID NO:217 Query: 484 TAAAEGTGKQVMHDPAMRPFMGMNFGRYMRHWMLGQPPHKVPKIF 530
SEQ ID NO:218 TAAAEGTGKQVMHDPAMRPFMGMNF+Y++HW+ L KV F
SEQ ID NO:219 Sbjct: 19576 TAAAEGTGKQVMHDPAMRPFMGMNFGRYQHLDLKTSRKVIDFF 19716

Score = 404 (187.6 bits), Expect = 0.0, Sum P(5) = 0.0
Identities = 68/116 (58%), Positives = 89/116 (76%), Frame = +1

SEQ ID NO:220 Query: 526 VPKIFHVNWFRQSAHKFLWPGYGDNIRVIDWILRRCSGDATAEETPIGFIPKKGTINL585
SEQ ID NO:221 +PKI+HVNWFR+ +++KFLWPG+GDNIRVIDWI+RR G+ I ETPIG +P KG+INL
SEQ ID NO:222 Sbjct: 19750 MPKIYHVNWFRKDSNNKFLWPGFGDNIRVIDWIIRRRLGEQEIGVETPIGTVPAKGSINL 19929

SEQ ID NO:220 Query: 586 EGLPNVNWDELMSIPKSYWLEDMVETKTFENQVGSDLPPEIAKELEAQTERIKAL 641
SEQ ID NO:221 EGL VNWDELMS+P YW +D E + F + QVG DLP + E++AQ +R++ L
SEQ ID NO:222 Sbjct: 19930 EGLGEVNWDELMSVPADYWKQDAQEIRKFLDEQVGEDLPEPVRAEMDAQEKRQVQTL 20097

Score = 69 (32.0 bits), Expect = 0.0, Sum P(5) = 0.0
Identities = 15/36 (41%), Positives = 21/36 (58%), Frame = +1

SEQ ID NO:223 Query: 5 SLSHFKDDDFAVVSEVVTHKQNHIPVIKGFVSLPK 40
SEQ ID NO:224 SL +D F VV+EVV + H+P++K F S K
SEQ ID NO:225 Sbjct: 14722 SLRQISEDAFYVVNEVVMKRLGHVPILKVFESSEK 14829

Score = 39 (18.1 bits), Expect = 6.9e-244, Sum P(4) = 6.9e-244
Identities = 9/25 (36%), Positives = 11/25 (44%), Frame = +3

SEQ ID NO:226 Query: 148 GCMAGRTMYVIPYSMGPVGGLSKI 172
SEQ ID NO:227 GC R + V P S PL K+
SEQ ID NO:228 Sbjct: 8040 GCSGRRVLCVCPCSHSSALPLQKV 8114

Score = 38 (17.6 bits), Expect = 4.0e-285, Sum P(5) = 4.0e-285
Identities = 7/16 (43%), Positives = 9/16 (56%), Frame = +1

SEQ ID NO:229 Query: 588 LPNVNWDELMSIPKSY 603
SEQ ID NO:230 L + NW +S P SY
SEQ ID NO:231 Sbjct: 22654 LESFNWFVFSCPDSY 22701

Score = 37 (17.2 bits), Expect = 2.0e-48, Sum P(3) = 2.0e-48
Identities = 6/14 (42%), Positives = 9/14 (64%), Frame = +1

SEQ ID NO:232 Query: 117 SVCHTPEGVKPMGG 130

SEQ ID NO:233 +V H P ++P MG
SEQ ID NO:234 Sbjct: 19603 TVMHDPMAMRPFMG 19644

Acetyl coa carboxylase

>W09B6

Length = 32,900

Plus Strand HSPs:

Score = 562 (259.1 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 109/197 (55%), Positives = 138/197 (70%), Frame = +2

SEQ ID NO:235 Query: 1951 SGFFDYGSFSEIMQPWAQTVVVGRARLGGIPVGVVAVETRTVELSVPADPANLDSEAKII 2010
SEQ ID NO:236 z +G D SF EI WA+++V GRARL GIP+GVV+ E R VPADPA S+ +
SEQ ID NO:237 Sbjct: 28280 TGICDTMSFDEICGDWAKSIVAGRARLCGIPIGVVSSEFRNFSTIVPADPAIDGSQVQNT 28459

SEQ ID NO:235 Query: 2011 QQAGQVWFPSAFKTYQAIAKDFNREGLPLMVFANWRGFSGGMKDMYDQVLKFGAYIVDGL 2070
SEQ ID NO:236 Q+AGQVW+PSAFKT +AI D N+E LPLM+ A+ RGFSGG KDMYD VLKFGA IVD L
SEQ ID NO:237 Sbjct: 28460 QRAGQVWYPDSAFKTAEEAINDLNKENLPLMIIASLRGFSGGQKDMYDMLVKFGAQIVDAL 28639

SEQ ID NO:235 Query: 2071 RECSQPVMVYIPPQAELRGGSWVVIDPTINPRHMEMYADRESRGSVLEPEGTVEIKFRKK 2130
SEQ ID NO:236 ++PV+VYIP ELRGG+W V+D I P + + AD +SRG +LEP V IKFRK
SEQ ID NO:237 Sbjct: 28640 AVYNRPVIVYIPEAGELRGGAWAVLDSKIRPEFIHLVADEKSRRGGILEPNAVVGKFRKP 28819

SEQ ID NO:235 Query: 2131 DLVKTMRVDPVYIRLA 2147
SEQ ID NO:236 +++ M+R DP Y +L+
SEQ ID NO:237 Sbjct: 28820 MMEMEMMKRSRDPYYSKLS 28870

Score = 357 (164.6 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 68/124 (54%), Positives = 89/124 (71%), Frame = +2

SEQ ID NO:238 Query: 303 VGYPVMIKASEGGGGKGIRKVNNADDFPNLFRQVQAEVPGSPIFVMRLAKQSRHLEVQIL 362
SEQ ID NO:239 +G+P+MIKASEGGGGKGIRK +DF ++F +V EV GSPIF+M+ +RH+EVQ+L
SEQ ID NO:240 Sbjct: 232641GFPMLIKASEGGGGKGIRKCTKVEDFKSMFEEVAQEVBQGSPIFLMKCVDGHARHIEVQLL 23443

SEQ ID NO:238 Query: 363 ADQYGNALSLFGRDCSVQRRHQKXXXXXXXXXXVFEHMEQCAVKLAKMVGYVSAGTV 422
SEQ ID NO:239 AD+Y N IS++ RDCS+QRR QK + + M++ AV+LAK VGY SAGTV
SEQ ID NO:240 Sbjct: 23444ADRYENVISVYTRDCSIQRRCQKIIIEAPAIASSHIRKSMQEDAVRLAKYVGYESAGTV 23623

SEQ ID NO:238 Query: 423 ELY 426
SEQ ID NO:239 ELY
SEQ ID NO:240 Sbjct: 23624 ELY 23635

Score = 345 (159.1 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 65/116 (56%), Positives = 86/116 (74%), Frame = +2

SEQ ID NO:241 Query: 1787 KEEGLGAENLRGSGMIAGESSLAYDEIITISLVTCRAIGIGAYLVRGQRTIQVENSHLI 1846
SEQ ID NO:242 K E +G ENL+GSG+IAGE++ AY E+ T VT R++GIGAY RL R +Q + SHLI
SEQ ID NO:243 Sbjct: 27794 KNEKIGVENLQGSGLIAGETARAYAEVPTCYVTPGRSGVGIGAYTARLAHRIVQHKQSHLI 27973

SEQ ID NO:241 Query: 1847 LTGAGALNKVLGREVYTSNNQLGGIQIMHNNGVTHCTVCDDFEGVFTVLHWLSYMP 1902
SEQ ID NO:242 LTG ALN +LG++VYTSNNQLGG ++M NGVTH V +D EG+ V+ W+S++P
SEQ ID NO:243 Sbjct: 27974 LTGYEALNTLLGKKVYTSNNQLGGPEVMFRNGVTHAVVDNDLEGIAKVIRWMSFLP 28141

Score = 319 (147.1 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 59/119 (49%), Positives = 80/119 (67%), Frame = +2

SEQ_ID NO:244 Query: 503 HVIAARITSEN PDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCF SW 562
SEQ_ID NO:245 H IAARIT ENPD+ F+PS+G V E+NF S+++ W YFSV +H+FADSFQGH F+
SEQ_ID NO:246 Sbjct: 23870 HAIAARITCENPDDSF RPSTGKVEINF PSSQDAWAYFSVGRGSSVHQFADSQFGHIFTR 24049

SEQ_ID NO:244 Query: 563 GENREEAISNMVALKELSIRGDRTTVEYLIKLLTEESFQLNRIDTGWLDRLLIAEKVQ 621
SEQ_ID NO:245 G +R EA++ M LK ++IR F T V YL+ L+ F N +T WLD+ IA K++
SEQ_ID NO:246 Sbjct: 24050 GTSRTEAMNTMCSTLKHM TIRSSFPQTQVNLYLV DLMHDADFINNAFTQWL DKRIAMKIK 24226

Score = 303 (139.7 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 55/90 (61%), Positives = 70/90 (77%), Frame = +2

SEQ_ID NO:247 Query: 178 PGGANNNNYANVELILDIAKRIPVQAVWAGWGHASENP KLP ELLKNGIAFMGPPSQAMW 237
SEQ_ID NO:248 P G N NN+ANV+ IL A + V AVWAGWGHASENP LP L + IAF+GPP+ AM+
SEQ_ID NO:249 Sbjct: 22886 PSGTNKNNFANVDEILKHAIKYEVDAVWAGWGHASENPDLPRRLNDHNIAFIGPPASAMF 23065

SEQ_ID NO:247 Query: 238 ALGDKIASSIVAQTAGIPTLPWSGSGLRVD 267
SEQ_ID NO:248 +LGDKIAS+I+AQT G+PT+ WSGSG+ ++
SEQ_ID NO:249 Sbjct: 23066 SLGDKIASTIIAQTVGVPTVAWSGSGITME 23155

Trehelase

>C23H3

Length = 39,721

Minus Strand HSPs:

Score = 227 (104.5 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 36/67 (53%), Positives = 51/67 (76%), Frame = -2

SEQ_ID NO:250 Query: 2 VIKNLGYMVDNHGFVPGNGRYYL TRSQPPLTPMV EYYMSTGDLDFVMEILPTLDKEY 61
SEQ_ID NO:251 +I N +++++ GFVPGNGRYYL RSQPP PMVY EYY++T D+ V +++P ++KEY
SEQ_ID NO:252 Sbjct: 9798 MILNFAHIIETYGFVPGNGRYYLRRSQPFFAPMVY EYYLATQDIQLVADLIPVIEKEY 9619

SEQ_ID NO:250 Query: 62 EFWIKNR 68
SEQ_ID NO:251 FW + R
SEQ_ID NO:252 Sbjct: 9618 TFWSER R 9598

Score = 182 (83.8 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 32/92 (34%), Positives = 55/92 (59%), Frame = -2

SEQ_ID NO:253 Query: 146 MDSIRTWSIIPADLN AFMCANARILASLYEIA GDFKKVKVFEQRYTWA KREMRELHWNET 205
SEQ_ID NO:254 + +I T +I+P DLNAF+C N I+ Y++ G+ K + R+T + ++ +
SEQ_ID NO:255 Sbjct: 9372 ISTIETTNIVPV DLN AFLCYN MNIM QLFYKLTGNPLKHL EWSSRFTNFRA EFTKVFYVPA 9193

SEQ_ID NO:253 Query: 206 DGIWYDYDIELKTHSNQYYVSNAVPLYAKCYD 237
SEQ_ID NO:254 WYDY++ TH+ ++ SNAVPL++CYD
SEQ_ID NO:255 Sbjct: 9192 RKGWYDYNLRTLTHNT DFFASNAVPLFSQCYD 9097

Score = 178 (81.9 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 37/102 (36%), Positives = 55/102 (53%), Frame = -2

SEQ_ID NO:256 Query: 246 VHDYLERQGLLK YT KGLPTSLAMS STQWD KENAW PPMI HMVIEG FR TTG DI KLMKVAEK 305
SEQ_ID NO:257 V++ ++ G G+PTS+ + QQWD N W PM HM+IEG R + + L + A
SEQ_ID NO:258 Sbjct: 9069 VYNEMQN SGA FSIPGGI PTSMNE ETNQQWDFPNGWSP MNHMIIEGLRK SNNPILQQKAFT 8890

SEQ_ID NO:256 Query: 306 MATSWLTGTYQS FIRTHAMFEKYNVTPH TEETSGGGGEYEV 347
SEQ_ID NO:257 +A WL Q+F + M+E KYNV + + GG E +V
SEQ_ID NO:258 Sbjct: 8889 LAEKWLET NMQTFNV SDEMWEKYNVKEPLGK LATGGEYEVQV 8764

Score = 169 (77.8 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 29/58 (50%), Positives = 41/58 (70%), Frame = -2

SEQ ID NO:259 Query: 84 YQYKAKLKVPKPESYREDSELAEHLQTEAEKIQMWSIEASAAETGWDFSTRWFQSQNGD 141
SEQ ID NO:260 +QY+ + + PRPES+RED AEH T+ K Q + ++ SAAE+GWDFS+RWF + D
SEQ ID NO:261 Sbjct: 9546 FQYRTEAETPRPESFREDVLSAEHFTTKDRKKQFFKDLGSAAESGWDFFSSRWFKNHKD 9373

Score = 76 (35.0 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 13/21 (61%), Positives = 15/21 (71%), Frame = -1

SEQ ID NO:262 Query: 348 QTGFQWTNGVILDLLDKYGDQ 368
SEQ ID NO:263 Q GFGWTNG LDL+ Y D+
SEQ ID NO:264 Sbjct: 8722 QAGFGWTNGAALDLIFTYSQR 8660

Score = 45 (20.7 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 10/24 (41%), Positives = 15/24 (62%), Frame = -1

SEQ ID NO:265 Query: 371 SSSTASKFSFSLSNITFVVFILYI 394
SEQ ID NO:266 +SS+S F +S VF+LYI
SEQ ID NO:267 Sbjct: 8545 TSSSSSTFGYSNILTLLITVFVLYI 8474

Score = 38 (17.5 bits), Expect = 2.6e-98, Sum P(7) = 2.6e-98
Identities = 7/7 (100%), Positives = 7/7 (100%), Frame = -2

SEQ ID NO:268 Query: 342 GGEYEVQ 348
SEQ ID NO:269 GGEYEVQ
SEQ ID NO:270 Sbjct: 8787 GGEYEVQ 8767

Score = 37 (17.0 bits), Expect = 1.6e-19, Sum P(4) = 1.6e-19
Identities = 8/18 (44%), Positives = 10/18 (55%), Frame = -2

SEQ ID NO:271 Query: 217 KTHSNQYYVSNAVPLYAK 234
SEQ ID NO:272 K ++ YYVS P Y K
SEQ ID NO:273 Sbjct: 30345 KFTAHPYYVSRTPPRYHK 30292

>W05E10

Length = 31,273

Minus Strand HSPs:

Score = 224 (103.1 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 43/67 (64%), Positives = 49/67 (73%), Frame = -1

SEQ ID NO:274 Query: 2 VIKNLGYMVDNHGFVPGNGGRVYYLTRSQPPLTTPMVYEYMMSTGDLDFVMEILPTLDKEY 61
SEQ ID NO:275 +I+NL MVD +GFVPGNGGRVYYL RSQPP L MVYE Y+ T D FV E+LPTL KE
SEQ ID NO:276 Sbjct: 28957MIRNLASMVDKYGFVPGNGGRVYYLQRSQPPFLAAMVYELYEAATNDKAFVAELLPTLLKEL28778

SEQ ID NO:274 Query: 62 EFWIKNR 68
SEQ ID NO:275 FW + R
SEQ ID NO:276 Sbjct: 28777 NFWNEKR 28757

Score = 192 (88.4 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 31/84 (36%), Positives = 52/84 (61%), Frame = -3

SEQ ID NO:277 Query: 154 IIPADLNFM CANARILASLYEIAGDFKKVKVFEQRYTWAKREMRELHWNETDGIWYDYD 213

SEQ ID NO:278 ++P DLN + C N I + LYE GD K ++F + + + + +N TDG WYDY+
SEQ ID NO:279 Sbjct: 2842 7VLPVDLNGLLCWNMDIMEYLYEQIGDTKNSQIFRNKRADFRDTVQNVFYNRDGTWYDYN 28248

SEQ ID NO:277 Query: 214 IELKTHSNQQYYVSNAVPLYAKCYD 237
SEQ ID NO:278 + ++H+ ++Y S AVPL+ CY+
SEQ ID NO:279 Sbjct: 28247 LRTQSHNPRFYTSTAVPLFTNCYN 28176

Score = 125 (57.5 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 20/48 (41%), Positives = 30/48 (62%), Frame = -2

SEQ ID NO 280 Query: 249 YLERQGLLKTYTKGLPTSLAMSSTQQWDKENAWPPMIHMVIEGFRTTG 296
SEQ ID NO 281 + ++ G+ Y G+PTS++ S QQWD N W P HM+IEG R + +
SEQ ID NO 282 Sbjct: 28092 FFQKMGVFTYPGGIPTSMSQESDQQWDFPNGWSPNNHMIIEGLRKSAN 27949

Score = 90 (41.4 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 15/18 (83%), Positives = 18/18 (100%), Frame = -2

SEQ ID NO 283 Query: 120 EIASAETGWFSTRWFS 137
SEQ ID NO 284 + +ASAAE+GWDFSTRWFS
SEQ ID NO 285 Sbjct: 28566 DLASAAESGWDFSTRWFS 28513

Score = 89 (41.0 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 18/40 (45%), Positives = 24/40 (60%), Frame = -1

SEQ ID NO 286 Query: 79 KQFPYYQYKAKLKVPVRPESYREDSELAEHLQTEAEKIQM 118
SEQ ID NO 287 K F YQYK VPRPESYR D++ + L A++ Q +
SEQ ID NO 288 Sbjct: 28732 KSFKVYQYKTASNVPVRPESYRVDTQNSAKLANGADQQQFY 28613

Score = 77 (35.4 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 14/21 (66%), Positives = 16/21 (76%), Frame = -3

SEQ ID NO 289 Query: 348 QTGFGWTNGVILDLLDKYGDQ 368
SEQ ID NO 290 Q GFGW+NG ILDLL Y D+
SEQ ID NO 291 Sbjct: 24395 QDGFGWSNGAILEDLLTYNDR 24333

Score = 51 (23.5 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 11/27 (40%), Positives = 16/27 (59%), Frame = -3

SEQ ID NO 292 Query: 365 YGDQFASSSTASKFSFSLSNITFVVFI 391
SEQ ID NO 293 Y FASSS AS FS +++ F + +
SEQ ID NO 294 Sbjct: 2846 YN*PFASSSDASSCPFSTNSVIFSILV 2766

Score = 41 (18.9 bits), Expect = 3.3e-93, Sum P(8) = 3.3e-93
Identities = 7/9 (77%), Positives = 8/9 (88%), Frame = -2

SEQ ID NO 295 Query: 340 GGGGEYEVQ 348
SEQ ID NO 296 G GGEY+VQ
SEQ ID NO 297 Sbjct: 24468 GSGGEYDVQ 24442

Score = 39 (18.0 bits), Expect = 2.0e-37, Sum P(5) = 2.0e-37
Identities = 7/14 (50%), Positives = 8/14 (57%), Frame = -2

SEQ ID NO 298 Query: 221 NQYYVSNAVPLYAK 234
SEQ ID NO 299 N YY+ V LY K
SEQ ID NO 300 Sbjct: 4524 NHYYIIQMVSLYTK 4483

Score = 38 (17.5 bits), Expect = 4.0e-88, Sum P(7) = 4.0e-88
Identities = 11/30 (36%), Positives = 13/30 (43%), Frame = -1

SEQ ID NO 301 Query: 367 DQFASSSTASKFSFSLSNITVVVILYIFS 396
SEQ ID NO 302 DQF S SKFS + F +FS
SEQ ID NO 303 Sbjct: 7588 DQFVISFICSKFSSKNKKLYFCPSHFSLFS 7499

In the Claims:

1. (Twice Amended) A method for identifying a compound that modulates DAF-18 expression or activity, comprising:

- (a) providing a nematode, isolated nematode cell, or isolated mammalian cell expressing a nematode *daf-18* gene; and
- (b) contacting said nematode, isolated nematode cell, or isolated mammalian cell with a candidate compound[, an alteration in] to determine the effect of said candidate compound on daf-18 expression or activity, an alteration in said daf-18 expression or activity following contact of said nematode, isolated nematode cell, or isolated mammalian cell with said candidate compound identifying said candidate compound as a modulatory compound.

2. (Twice Amended) A method for identifying a compound that modulates PTEN expression or activity, comprising:

- (a) providing a nematode or isolated nematode cell comprising a mutation in its endogenous *daf-18* gene;
- (b) expressing in said nematode or isolated nematode cell a mammalian PTEN gene; and
- (c) contacting said nematode or isolated nematode cell with a candidate compound[, an alteration in] to determine the effect of said candidate compound on PTEN expression or activity, an alteration in said PTEN expression or activity following contact with said candidate compound identifying said candidate compound as a modulatory compound.